

Application No. 09/823,649

Appendix B

(4 pages)

Get Nucleotide sequences for Site search Database
Site Map
EBI Queries

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Databases

Documentation

FTP site

Protein of the month

InterPro

InterPro home	Text Search	Sequence Search	Databases	Documentation	FTP site	Protein of the month
Search: <input type="text"/>				Search Entries		

Simple | Full HTML Version
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InterPro Protein matches

Select:	Protein accession(s)	<input checked="" type="checkbox"/> P00582
Refine:	Proteins with alternative splicing:	<input type="checkbox"/>
	Proteins with known structure:	<input type="checkbox"/>
	Taxonomy - NCBI tax ID(s):	
Display:	Detailed	<input checked="" type="checkbox"/>
Sort:	Accession	<input checked="" type="checkbox"/>

Taxonomy Lineage

no rank: Root node of taxonomy 1
no rank:
cellular organisms 1

Protein Match data

DNA polymerase I (EC 2.7.7.7) (POL I)















- [Table of Matches](#)
- [GO annotation](#)
- [View protein UniProt information](#)











IPR001098	IPR001098	IPR001098	IPR002298	IPR002298	IPR002421	IPR002421	IPR002421	IPR002562	IPR002562	IPR003583	IPR008918
PF00476	PS00447	SM00482	PR00868	TIGR00593	PF01367	PF02739	SM00475	SM00474	SM00278	SM00279	SS1
			655-677 T								
			678-693 T								
			700-723 T								
			730-743 T								
547-927 T	754-773 T	686-892 T	754-779 T	9-928 T	171-277 T	7-169 T	7-268 T	330-517 T	188-207 T	173-208 T	179
			791-802 T								
			813-824 T								
			845-861 T								
			875-888 T								
InterPro Signatures											
IPR001098	PF00476										
IPR001098	PS00447										
IPR001098	SM00482										
IPR002298	PR00868										
IPR002298	TIGR00593										
IPR002421	PF01367										
IPR002421	PF02739										
IPR002421	SM00475										
IPR002562	PF01612										
IPR002562	SM00474										

UniProt :
P00582
Scale:10aa
DPO1_ECOLI




Structure:
GO:
Escherichia coli

IPR003583	SM00278	
IPR008918	SM00279	
IPR008918	SSF47807	
IPR012337	SSF53098	
Structural features 		
1dpl	1dpl	
1.10.150.20.17	2kna4	
1.20.1060.10.1	2kna2	
3.30.420.10.16	2kna1	
3.30.70.370.1	2kna3	
c.55.3.5	d2kna1	
e.8.1.1	d2kna2	
Structural predictions 		
MB_P00582		

ModBase	
PRINTS	
Plam	
PROSITE pattern	
SMART	
SuperFamily	
PDB Chain	

Match Status key: 	
T	True

CATH Domain		F	False
TIGRFAMs		P	Partial
SCOP Domain		U	Unknown
		N	False negative

IPR001098	DNA-directed DNA polymerase	
IPR002421	5'-3' exonuclease	
IPR002562	3'-5' exonuclease	

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InterPro 12.1

[Stat]

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